

SEQUENCE LISTING

<110> ITO, Yasuaki
FUJII, Ryo
KOBAYASHI, Makoto
HINUMA, Shuji
HASHIMOTO, Tadatoshi
TANAKA, Yasuhiro

<120> Novel Screening Method

<130> 3172USOP

<140> 10/552,014

<141> 2005-10-12

<150> PCT/JP2004/005947

<151> 2004-04-23

<150> JP 2003-122464

<151> 2003-04-25

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<211> 453

<212> PRT

<213> Human

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	245		250	255
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	260		265	270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile				
	275		280	285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile				
	290		295	300
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Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser				320
	325		330	335
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	340		345	350
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala				
	355		360	365
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser				
	370		375	380
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser				
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Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu				400
	405		410	415
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<211> 456
<212> PRT
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          20              25              30
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          35              40              45
Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
          50              55              60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
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Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
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Leu	Ser	Phe	Glu	Arg	Tyr	Ile	Ala	Ile	Cys	His	Pro	Phe	Lys	Tyr	Lys
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		195					200					205			
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Met	Cys	Trp	Asn	Met	Met	Lys	Val	Leu	Met	Lys	Ser	Lys	Gln	Gly	Thr
			245					250						255	
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Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
                50              55              60
Gln Lys Glu Val Thr Asp His Met Ile Ser Leu Ala Cys Ser Asp Ile
                65              70              75              80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
                85              90              95
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Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
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Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
                130             135             140
Asp Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
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Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
                165             170             175
Glu Tyr Pro Leu Ala Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
                180             185             190
Leu Ser Arg Thr Arg His His Asp His Pro Gly Asp Ser Asn Met Ser
                195             200             205
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Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Val Ser Val Ala Phe

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	260	265	270			
Glu Ser Arg Thr	Ala Arg Arg Gln	Thr Ile Ile Phe	Leu Arg Leu Ile			
	275	280	285			
Val Val Thr Leu	Ala Val Cys Trp	Met Pro Asn Gln	Ile Arg Arg Ile			
	290	295	300			
Met Ala Ala Ala	Lys Pro Lys His	Asp Trp Thr Lys	Ser Tyr Phe Lys			
305	310	315	320			
Ala Tyr Met Ile	Leu Leu Pro Phe	Ser Asp Thr Phe	Phe Tyr Leu Ser			
	325	330	335			
Ser Val Val Asn	Pro Leu Leu Tyr	Asn Val Ser Ser	Gln Gln Phe Arg			
	340	345	350			
Lys Val Phe Trp	Gln Val Leu Cys	Cys Arg Leu Thr	Leu Gln His Ala			
	355	360	365			
Asn Gln Glu Lys	Gln Gln Arg Ala	Tyr Phe Ser Ser	Thr Lys Asn Ser			
	370	375	380			
Ser Arg Ser Ala	Arg Ser Pro Leu	Ile Phe Leu Ala	Ser Arg Arg Ser			
385	390	395	400			
Asn Ser Ser Ser	Arg Arg Thr Asn	Lys Val Phe Leu	Ser Thr Phe Gln			
	405	410	415			
Ala Glu Ala Lys	Pro Leu Glu Gly	Glu His Gln Pro	Leu Ser Pro Glu			
	420	425	430			
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Asn Ser Leu Gln	Glu Gln Glu Val					
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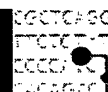



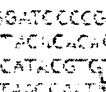
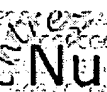


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[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

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Limits Preview/Index History Clipboard Details

Display Show

Range: from to ☐ Reverse complemented strand Features: ☐ SNP ☒ CDD ☐

☐ 1: [XM_222578](#). Reports PREDICTED: Rattus...[gi:34879487]

[Links](#)

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LOCUS XM_222578 1371 bp mRNA linear ROD 15-APR-2005
 DEFINITION PREDICTED: Rattus norvegicus G protein-coupled receptor 39
 (predicted) (Gpr39_predicted), mRNA.
 ACCESSION XM_222578
 VERSION XM_222578.2 GI:34879487
 KEYWORDS .
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM [Rattus norvegicus](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational
 analysis. This record is derived from an annotated genomic sequence
 (NW_047393) using gene prediction method: GNOMON, supported by mRNA
 evidence.
 Also see:

[Documentation](#) of NCBI's Annotation Process

On Sep 22, 2003 this sequence version replaced gi:27676303.

FEATURES Location/Qualifiers
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LQEQEV"

ORIGIN

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```

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